

Query Match 100.0%; Score 7; DB 11; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKRILHC 7  
 |||||  
 Db 274 KKRILHC 280

## RESULT 2

ID Q9BRW8 PRELIMINARY; PRT; 296 AA.  
 AC Q9BRW8  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE SIMILAR TO BILIVERDIN REDUCTASE A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRIN;  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC005902; AAH05902.1;  
 SQ SEQUENCE 296 AA; 33432 MW; A389AFDD6ADB6B CRC64;

Query Match 100.0%; Score 7; DB 4; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 2.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKRILHC 7  
 |||||  
 Db 275 KKRILHC 281

## RESULT 3

ID Q9DD21 PRELIMINARY; PRT; 303 AA.  
 AC Q9DD21  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE 0610006A11RIK PROTEIN.  
 GN 0610006A11RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
 RX MEDLINE=21083660; PubMed=112717851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Saki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK002231; BAB21950.1;  
 DR MGD; MGI:1915580; 0610006A11RIK.  
 DR InterPro; IPR000683; GFO\_IDH\_MOCA.  
 DR Pfam; PF01408; GFO\_IDH\_MOCA; I.  
 SQ SEQUENCE 303 AA; 34491 MW; 52D8A3B02EE956EB CRC64;

Query Match 100.0%; Score 7; DB 11; Length 303;  
 Best Local Similarity 100.0%; Pred. No. 2.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKRILHC 7  
 |||||  
 Db 274 KKRILHC 280

## RESULT 4

ID Q32948 PRELIMINARY; PRT; 42 AA.  
 AC Q32948  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE ORF42A.  
 GN PSAM.  
 OS Pinus thunbergii (Green pine) (Japanese black pine).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=3350;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92212283; PubMed=1557027;  
 RA Tsudzuki J., Nakashima K., Tsudzuki T., Hiratsuka J., Shibata M.,  
 RA Wakasugi T., Sugiura M.;  
 RT "Chloroplast DNA of black pine retains a residual inverted repeat  
 RT lacking rRNA genes: nucleotide sequences of trnQ, trnK, psbA, trnI and  
 RT trnH and the absence of rps16.";  
 RL Mol. Gen. Genet. 232:206-214(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95094312; PubMed=8001170;  
 RA Tsudzuki J., Ito S., Tsudzuki T., Wakasugi T., Sugiura M.;  
 RT "A new gene encoding tRNA(Pro) (GGG) is present in the chloroplast  
 RT genome of black pine: a compilation of 32 tRNA genes from black pine  
 RT chloroplasts.";  
 RL Curr. Genet. 26:153-158(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95024047; PubMed=7937893;  
 RA Wakasugi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,  
 RA Sugiura M.;  
 RT "Loss of all ndh genes as determined by sequencing the entire  
 RT chloroplast genome of the black pine Pinus thunbergii.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798(1994).  
 DR EMBL; D17510; BAA04352.1;  
 KW Chloroplast.  
 SQ SEQUENCE 42 AA; 4972 MW; 9B06BE464A5F8565 CRC64;

Query Match 85.7%; Score 6; DB 8; Length 42;  
 Best Local Similarity 100.0%; Pred. No. 5.8;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KKRILH 6  
 |||||  
 Db 30 KKRILH 35